

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 09/674,377C  
Source: TFW16  
Date Processed by STIC: 09/21/2006

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

**SERIAL NUMBER: 09/674,377C**

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	
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**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4  Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11  Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/674,377C**

**DATE: 09/21/2006**  
**TIME: 11:21:18**

**Input Set : A:\Q61434.ST25.txt**  
**Output Set: N:\CRF4\09212006\I674377C.raw**

3 <110> APPLICANT: NAKAMURA, Toshikazu  
 5 <120> TITLE OF INVENTION: Neovascularization Inhibitors Derived From HGF and Methods  
 6 Involving The Same (as amended)  
 8 <130> FILE REFERENCE: Q61434  
 10 <140> CURRENT APPLICATION NUMBER: 09/674,377C  
 11 <141> CURRENT FILING DATE: 2000-10-30  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01834  
 14 <151> PRIOR FILING DATE: 1999-04-06  
 16 <150> PRIOR APPLICATION NUMBER: JPA 1998-134681  
 17 <151> PRIOR FILING DATE: 1998-04-28  
 19 <160> NUMBER OF SEQ ID NOS: 3  
 21 <170> SOFTWARE: PatentIn version 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 447  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: MOD\_RES  
 31 <222> LOCATION: (1)..(1)  
 32 <223> OTHER INFORMATION: pyroglutamate  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CHAIN  
 36 <222> LOCATION: (1)..(447)  
 37 <223> OTHER INFORMATION: N-Terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)  
 39 <400> SEQUENCE: 1  
 41 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys  
 42 1 5 10 15  
 45 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
 46 20 25 30  
 49 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
 50 35 40 45  
 53 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
 54 50 55 60  
 57 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
 58 65 70 75 80  
 61 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
 62 85 90 95  
 65 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr  
 66 100 105 110  
 69 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu  
 70 115 120 125  
 73 His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn  
 74 130 135 140

Does Not Comply  
 Corrected Diskette Needed  
 (pg-2,4)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/674,377C

DATE: 09/21/2006  
TIME: 11:21:18

Input Set : A:\Q61434.ST25.txt  
Output Set: N:\CRF4\09212006\I674377C.raw

77 Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr  
78 145 150 155 160  
81 Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser  
82 165 170 175  
85 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met  
86 180 185 190  
89 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr  
90 195 200 205  
93 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe  
94 210 215 220  
97 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys  
98 225 230 235 240  
101 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr  
102 245 250 255  
105 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr  
106 260 265 270  
109 Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr  
110 275 280 285  
113 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His  
114 290 295 300  
117 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu  
118 305 310 315 320  
121 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr  
122 325 330 335  
125 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys  
126 340 345 350  
129 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr  
130 355 360 365  
133 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp  
134 370 375 380  
137 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp  
138 385 390 395 400  
141 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala  
142 405 410 415  
145 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr  
146 420 425 430  
149 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
150 435 440 445

153 <210> SEQ ID NO: 2

154 <211> LENGTH: 442

155 <212> TYPE: PRT

156 <213> ORGANISM: 5 amino acid deletion

159 <220> FEATURE:

160 <221> NAME/KEY: MOD\_RES

161 <222> LOCATION: (1)..(1)

162 <223> OTHER INFORMATION: pyroglutamate

164 <220> FEATURE:

165 <221> NAME/KEY: CHAIN

166 <222> LOCATION: (1)..(442)

→ Invalid Response.  
<213> Responses can  
be either Artificial,  
Unknown or Genus species.  
See Item 10 on  
Error Summary  
Sheet.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,377C

DATE: 09/21/2006

TIME: 11:21:19

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw

167 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)

169 &lt;400&gt; SEQUENCE: 2

171 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys  
 172 1 5 10 15  
 175 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
 176 20 25 30  
 179 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
 180 35 40 45  
 183 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
 184 50 55 60  
 187 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
 188 65 70 75 80  
 191 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
 192 85 90 95  
 195 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr  
 196 100 105 110  
 199 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu  
 200 115 120 125  
 203 His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro  
 204 130 135 140  
 207 Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val  
 208 145 150 155 160  
 211 Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met  
 212 165 170 175  
 215 Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser  
 216 180 185 190  
 219 Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys  
 220 195 200 205  
 223 Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys  
 224 210 215 220  
 227 Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro  
 228 225 230 235 240  
 231 His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr  
 232 245 250 255  
 235 Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly  
 236 260 265 270  
 239 Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile  
 240 275 280 285  
 243 Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr  
 244 290 295 300  
 247 Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn  
 248 305 310 315 320  
 251 Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile  
 252 325 330 335  
 255 Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly  
 256 340 345 350  
 259 Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser  
 260 355 360 365  
 263 Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/674,377C

DATE: 09/21/2006  
TIME: 11:21:19

Input Set : A:\Q61434.ST25.txt  
Output Set: N:\CRF4\09212006\I674377C.raw

264 370 375 380  
267 Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn  
268 385 390 395 400  
271 Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys  
272 405 410 415  
275 Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg  
276 420 425 430  
279 Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
280 435 440  
283 <210> SEQ ID NO: 3  
284 <211> LENGTH: 10  
285 <212> TYPE: PRT  
286 <213> ORGANISM: amino acids 2-11 of human HGF alpha chain  
288 <400> SEQUENCE: 3  
290 Arg Lys Arg Arg Asn Thr Ile His Glu Phe  
291 1 5 10

See Glen 10  
on Error  
Summary  
Sheet.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/674,377C

DATE: 09/21/2006

TIME: 11:21:20

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw